

O P E

APR 25 2005

<110> SOONER TRADEMARK

SEQUENCE LISTING

<120> GLUCOSE DEHYDROGENASE BETA-SUBUNIT AND  
DNA ENCODING THE SAME

<130> TOYA126.002APC

<140> 10/511,796

<141> 2004-10-19

<150> PCT/JP03/05375

<151> 2003-04-25

<150> JP 2002-125353

<151> 2002-04-26

<160> 19

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2467

<212> DNA

<213> Burkholderia cepacia

<220>

<221> CDS

<222> (258) ... (761)

<221> CDS

<222> (764) ... (2380)

<221> CDS

<222> (2386) ... (2466)

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tagaaatggc tgacacatttgc aatggactat aaaaccatttgc tccgttccgg aatgtgcgcg 180  
tacatttcag gtccgcgcgcg atttttgaga aatatcaagc gtggtttcc cgaatccgg 240  
gttcgagaga aggaaac atg cac aac gac aac act ccc cac tcg cgt cgc 290  
Met His Asn Asp Asn Thr Pro His Ser Arg Arg

1 5 10

cac ggc gac gca gcc gca tca ggc atc acg cgg cgt caa tgg ttg caa 338  
His Gly Asp Ala Ala Ala Ser Gly Ile Thr Arg Arg Gln Trp Leu Gln  
15 20 25

ggc gcg ctg gcg ctg acc gca gcg ggc ctc acg ggt tcg ctg aca ttg 386  
Gly Ala Leu Ala Leu Thr Ala Ala Gly Leu Thr Gly Ser Leu Thr Leu  
30 35 40

cgg gcg ctt gca gac aac ccc ggc act gcg ccg ctc gat acg ttc atg 434  
Arg Ala Leu Ala Asp Asn Pro Gly Thr Ala Pro Leu Asp Thr Phe Met

45

50

55

acg ctt tcc gaa tcg ctg acc ggc aag aaa ggg ctc agc cgc gtg atc 482  
 Thr Leu Ser Glu Ser Leu Thr Gly Lys Lys Gly Leu Ser Arg Val Ile  
 60 65 70 75

ggc gag cgc ctg ctg cag gcg ctg cag aag ggc tcg ttc aag acg gcc 530  
 Gly Glu Arg Leu Leu Gln Ala Leu Gln Lys Gly Ser Phe Lys Thr Ala  
 80 85 90

gac agc ctg ccg cag ctc gcc ggc gcg ctc gcg tcc ggt tcg ctg acg 578  
 Asp Ser Leu Pro Gln Leu Ala Gly Ala Leu Ala Ser Gly Ser Leu Thr  
 95 100 105

cct gaa cag gaa tcg ctc gca ctg acg atc ctc gag gcc tgg tat ctc 626  
 Pro Glu Gln Glu Ser Leu Ala Leu Thr Ile Leu Glu Ala Trp Tyr Leu  
 110 115 120

ggc atc gtc gac aac gtc gtg att acg tac gag gaa gca tta atg ttc 674  
 Gly Ile Val Asp Asn Val Val Ile Thr Tyr Glu Glu Ala Leu Met Phe  
 125 130 135

ggc gtc gtg tcc gat acg ctc gtg atc cgt tcg tat tgc ccc aac aaa 722  
 Gly Val Val Ser Asp Thr Leu Val Ile Arg Ser Tyr Cys Pro Asn Lys  
 140 145 150 155

ccc ggc ttc tgg gcc gac aaa ccg atc gag agg caa gcc tg atg gcc 769  
 Pro Gly Phe Trp Ala Asp Lys Pro Ile Glu Arg Gln Ala Met Ala  
 160 165 170

gat acc gat acg caa aag gcc gac gtc gtc gtc gtt gga tcg ggt gtc 817  
 Asp Thr Asp Thr Gln Lys Ala Asp Val Val Val Val Gly Ser Gly Val  
 175 180 185

gcg ggc gcg atc gtc gcg cat cag ctc gcg atg gcg ggc aag gcg gtg 865  
 Ala Gly Ala Ile Val Ala His Gln Leu Ala Met Ala Gly Lys Ala Val  
 190 195 200

atc ctg ctc gaa gcg ggc ccg cgc atg ccg cgc tgg gaa atc gtc gag 913  
 Ile Leu Leu Glu Ala Gly Pro Arg Met Pro Arg Trp Glu Ile Val Glu  
 205 210 215

cgc ttc cgc aat cag ccc gac aag atg gac ttc atg gcg ccg tac ccg 961  
 Arg Phe Arg Asn Gln Pro Asp Lys Met Asp Phe Met Ala Pro Tyr Pro  
 220 225 230

tcg agc ccc tgg gcg ccg cat ccc gag tac ggc ccg ccg aac gac tac 1009  
 Ser Ser Pro Trp Ala Pro His Pro Glu Tyr Gly Pro Pro Asn Asp Tyr  
 235 240 245 250

ctg atc ctg aag ggc gag cac aag ttc aac tcg cag tac atc cgc gcg 1057  
 Leu Ile Leu Lys Gly Glu His Lys Phe Asn Ser Gln Tyr Ile Arg Ala  
 255 260 265

gtg ggc ggc acg acg tgg cac tgg gcc gcg tcg gcg tgg ccg ttc att 1105  
 Val Gly Gly Thr Thr Trp His Trp Ala Ala Ser Ala Trp Arg Phe Ile  
 270 275 280

ccg aac gac ttc aag atg aag agc gtg tac ggc gtc ggc cgc gac tgg		1153
Pro Asn Asp Phe Lys Met Lys Ser Val Tyr Gly Val Gly Arg Asp Trp		
285	290	295
ccg atc cag tac gac gat ctc gag ccg tac tat cag cgc gcg gag gaa		1201
Pro Ile Gln Tyr Asp Asp Leu Glu Pro Tyr Tyr Gln Arg Ala Glu Glu		
300	305	310
gag ctc ggc gtg tgg ggc ccg ggc ccc gag gaa gat ctg tac tcg ccg		1249
Glu Leu Gly Val Trp Gly Pro Gly Pro Glu Glu Asp Leu Tyr Ser Pro		
315	320	325
330		
ccg aag cag ccg tat ccg atg ccg ccg ctg ccg ttg tcg ttc aac gag		1297
Arg Lys Gln Pro Tyr Pro Met Pro Leu Pro Leu Ser Phe Asn Glu		
335	340	345
cag acc atc aag acg gcg ctg aac aac tac gat ccg aag ttc cat gtc		1345
Gln Thr Ile Lys Thr Ala Leu Asn Asn Tyr Asp Pro Lys Phe His Val		
350	355	360
gtg acc gag ccg gtc gcg ccg aac agc ccg ccg tac gac ggc cgc ccg		1393
Val Thr Glu Pro Val Ala Arg Asn Ser Arg Pro Tyr Asp Gly Arg Pro		
365	370	375
act tgt tgc ggc aac aac aac tgc atg ccg atc tgc ccg atc ggc gcg		1441
Thr Cys Cys Gly Asn Asn Asn Cys Met Pro Ile Cys Pro Ile Gly Ala		
380	385	390
atg tac aac ggc atc gtc cac gtc gag aag gcc gaa cgc gcc ggc gcg		1489
Met Tyr Asn Gly Ile Val His Val Glu Lys Ala Glu Arg Ala Gly Ala		
395	400	405
410		
aag ctg atc gag aac gcg gtc gtc tac aag ctc gag acg ggc ccg gac		1537
Lys Leu Ile Glu Asn Ala Val Val Tyr Lys Leu Glu Thr Gly Pro Asp		
415	420	425
425		
aag cgc atc gtc gcg ccg ctc tac aag gac aag acg ggc gcc gag cat		1585
Lys Arg Ile Val Ala Ala Leu Tyr Lys Asp Lys Thr Gly Ala Glu His		
430	435	440
440		
ccg gtc gaa ggc aag tat ttc gtg ctc gcc gcg aac ggc atc gag acg		1633
Arg Val Glu Gly Lys Tyr Phe Val Leu Ala Ala Asn Gly Ile Glu Thr		
445	450	455
455		
ccg aag atc ctg ctg atg tcc gcg aac ccg gat ttc ccg aac ggt gtc		1681
Pro Lys Ile Leu Leu Met Ser Ala Asn Arg Asp Phe Pro Asn Gly Val		
460	465	470
470		
gcg aac agc tcg gac atg gtc ggc ccg aac ctg atg gac cat ccg ggc		1729
Ala Asn Ser Ser Asp Met Val Gly Arg Asn Leu Met Asp His Pro Gly		
475	480	485
485		
490		
acc ggc gtg tcg ttc tat gcg agc gag aag ctg tgg ccg ggc ccg ggc		1777
Thr Gly Val Ser Phe Tyr Ala Ser Glu Lys Leu Trp Pro Gly Arg Gly		
495	500	505
505		

ccg cag gag atg acg tcg ctg atc ggt ttc cgc gac ggt ccg ttc cgc		1825	
Pro Gln Glu Met Thr Ser Leu Ile Gly Phe Arg Asp Gly Pro Phe Arg			
510	515	520	
gcg acc gaa gcg gcg aag aag atc cac ctg tcg aac ctg tcg cgc atc		1873	
Ala Thr Glu Ala Ala Lys Lys Ile His Leu Ser Asn Leu Ser Arg Ile			
525	530	535	
gac cag gag acg cag aag aag atc ttc aag gcc ggc aag ctg atg aag ccc		1921	
Asp Gln Glu Thr Gln Lys Ile Phe Lys Ala Gly Lys Leu Met Lys Pro			
540	545	550	
gac gag ctc gac gcg cag atc cgc gac cgt tcc gca cgc tac gtg cag		1969	
Asp Glu Leu Asp Ala Gln Ile Arg Asp Arg Ser Ala Arg Tyr Val Gln			
555	560	565	570
ttc gac tgc ttc cac gaa atc ctg ccg caa ccc gag aac cgc atc gtg		2017	
Phe Asp Cys Phe His Glu Ile Leu Pro Gln Pro Glu Asn Arg Ile Val			
575	580	585	
ccg agc aag acg gcg acc gat gcg atc ggc att ccg cgc ccc gag atc		2065	
Pro Ser Lys Thr Ala Thr Asp Ala Ile Gly Ile Pro Arg Pro Glu Ile			
590	595	600	
acg tat gcg atc gac gac tac gtg aag cgc ggc gcc gcg cat acg cgc		2113	
Thr Tyr Ala Ile Asp Asp Tyr Val Lys Arg Gly Ala Ala His Thr Arg			
605	610	615	
gag gtc tac gcg acc gcc gcg aag gtg ctc ggc ggc acg gac gtc gtg		2161	
Glu Val Tyr Ala Thr Ala Ala Lys Val Leu Gly Gly Thr Asp Val Val			
620	625	630	
ttc aac gac gaa ttc gcg ccg aac aat cac atc acg ggc tcg acg atc		2209	
Phe Asn Asp Glu Phe Ala Pro Asn Asn His Ile Thr Gly Ser Thr Ile			
635	640	645	650
atg ggc gcc gat gcg cgc gac tcc gtc gtc gac aag gac tgc cgc acg		2257	
Met Gly Ala Asp Ala Arg Asp Ser Val Val Asp Lys Asp Cys Arg Thr			
655	660	665	
ttc gac cat ccg aac ctg ttc att tcg acg acg gcg acg atg ccg acc		2305	
Phe Asp His Pro Asn Leu Phe Ile Ser Ser Ser Ala Thr Met Pro Thr			
670	675	680	
gtc ggt acc gta aac gtg acg ctg acg atc gcc gcg ctc gcg ctg cgg		2353	
Val Gly Thr Val Asn Val Thr Leu Thr Ile Ala Ala Leu Ala Leu Arg			
685	690	695	
atg tcg gac acg ctg aag aag gaa gtc tgacc gtg cgg aaa tct act ctc		2403	
Met Ser Asp Thr Leu Lys Lys Glu Val Val Arg Lys Ser Thr Leu			
700	705	710	
act ttc ctc atc gcc ggc tgc ctc gcg ttg ccg ggc ttc gcg cgc gcg		2451	
Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu Pro Gly Phe Ala Arg Ala			
715	720	725	
gcc gat gcg gcc gat c		2467	

Ala Asp Ala Ala Asp  
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<210> 2  
<211> 168  
<212> PRT  
<213> Burkholderia cepacia

<400> 2  
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Thr Ala Ala Gly Leu Thr Gly Ser Leu Thr Leu Arg Ala Leu Ala Asp  
35 40 45  
Asn Pro Gly Thr Ala Pro Leu Asp Thr Phe Met Thr Leu Ser Glu Ser  
50 55 60  
Leu Thr Gly Lys Lys Gly Leu Ser Arg Val Ile Gly Glu Arg Leu Leu  
65 70 75 80  
Gln Ala Leu Gln Lys Gly Ser Phe Lys Thr Ala Asp Ser Leu Pro Gln  
85 90 95  
Leu Ala Gly Ala Leu Ala Ser Gly Ser Leu Thr Pro Glu Gln Glu Ser  
100 105 110  
Leu Ala Leu Thr Ile Leu Glu Ala Trp Tyr Leu Gly Ile Val Asp Asn  
115 120 125  
Val Val Ile Thr Tyr Glu Glu Ala Leu Met Phe Gly Val Val Ser Asp  
130 135 140  
Thr Leu Val Ile Arg Ser Tyr Cys Pro Asn Lys Pro Gly Phe Trp Ala  
145 150 155 160  
Asp Lys Pro Ile Glu Arg Gln Ala  
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<210> 3  
<211> 539  
<212> PRT  
<213> Burkholderia cepacia

<400> 3  
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35 40 45  
Val Glu Arg Phe Arg Asn Gln Pro Asp Lys Met Asp Phe Met Ala Pro  
50 55 60  
Tyr Pro Ser Ser Pro Trp Ala Pro His Pro Glu Tyr Gly Pro Pro Asn  
65 70 75 80  
Asp Tyr Leu Ile Leu Lys Gly Glu His Lys Phe Asn Ser Gln Tyr Ile  
85 90 95  
Arg Ala Val Gly Gly Thr Thr Trp His Trp Ala Ala Ser Ala Trp Arg  
100 105 110  
Phe Ile Pro Asn Asp Phe Lys Met Lys Ser Val Tyr Gly Val Gly Arg  
115 120 125  
Asp Trp Pro Ile Gln Tyr Asp Asp Leu Glu Pro Tyr Tyr Gln Arg Ala

130	135	140													
Glu	Glu	Leu	Gly	Val	Trp	Gly	Pro	Gly	Pro	Glu	Glu	Asp	Leu	Tyr	
145				150			155						160		
Ser	Pro	Arg	Lys	Gln	Pro	Tyr	Pro	Met	Pro	Pro	Leu	Pro	Leu	Ser	Phe
				165				170					175		
Asn	Glu	Gln	Thr	Ile	Lys	Thr	Ala	Leu	Asn	Asn	Tyr	Asp	Pro	Lys	Phe
				180				185					190		
His	Val	Val	Thr	Glu	Pro	Val	Ala	Arg	Asn	Sér	Arg	Pro	Tyr	Asp	Gly
				195				200				205			
Arg	Pro	Thr	Cys	Cys	Gly	Asn	Asn	Asn	Cys	Met	Pro	Ile	Cys	Pro	Ile
				210				215				220			
Gly	Ala	Met	Tyr	Asn	Gly	Ile	Val	His	Val	Glu	Lys	Ala	Glu	Arg	Ala
				225				230			235		240		
Gly	Ala	Lys	Leu	Ile	Glu	Asn	Ala	Val	Val	Tyr	Lys	Leu	Glu	Thr	Gly
				245				250					255		
Pro	Asp	Lys	Arg	Ile	Val	Ala	Ala	Leu	Tyr	Lys	Asp	Lys	Thr	Gly	Ala
				260				265					270		
Glu	His	Arg	Val	Glu	Gly	Lys	Tyr	Phe	Val	Leu	Ala	Ala	Asn	Gly	Ile
				275				280				285			
Glu	Thr	Pro	Lys	Ile	Leu	Leu	Met	Ser	Ala	Asn	Arg	Asp	Phe	Pro	Asn
				290				295				300			
Gly	Val	Ala	Asn	Ser	Ser	Asp	Met	Val	Gly	Arg	Asn	Leu	Met	Asp	His
				305				310			315		320		
Pro	Gly	Thr	Gly	Val	Ser	Phe	Tyr	Ala	Ser	Glu	Lys	Leu	Trp	Pro	Gly
				325				330					335		
Arg	Gly	Pro	Gln	Glu	Met	Thr	Ser	Leu	Ile	Gly	Phe	Arg	Asp	Gly	Pro
				340				345					350		
Phe	Arg	Ala	Thr	Glu	Ala	Ala	Lys	Lys	Ile	His	Leu	Ser	Asn	Leu	Ser
				355				360					365		
Arg	Ile	Asp	Gln	Glu	Thr	Gln	Lys	Ile	Phe	Lys	Ala	Gly	Lys	Leu	Met
				370				375				380			
Lys	Pro	Asp	Glu	Leu	Asp	Ala	Gln	Ile	Arg	Asp	Arg	Ser	Ala	Arg	Tyr
				385				390			395		400		
Val	Gln	Phe	Asp	Cys	Phe	His	Glu	Ile	Leu	Pro	Gln	Pro	Glu	Asn	Arg
				405				410					415		
Ile	Val	Pro	Ser	Lys	Thr	Ala	Thr	Asp	Ala	Ile	Gly	Ile	Pro	Arg	Pro
				420				425					430		
Glu	Ile	Thr	Tyr	Ala	Ile	Asp	Asp	Tyr	Val	Lys	Arg	Gly	Ala	Ala	His
				435				440					445		
Thr	Arg	Glu	Val	Tyr	Ala	Thr	Ala	Ala	Lys	Val	Leu	Gly	Gly	Thr	Asp
				450				455				460			
Val	Val	Phe	Asn	Asp	Glu	Phe	Ala	Pro	Asn	Asn	His	Ile	Thr	Gly	Ser
				465				470			475		480		
Thr	Ile	Met	Gly	Ala	Asp	Ala	Arg	Asp	Ser	Val	Val	Asp	Lys	Asp	Cys
				485				490					495		
Arg	Thr	Phe	Asp	His	Pro	Asn	Leu	Phe	Ile	Ser	Ser	Ala	Thr	Met	
				500				505					510		
Pro	Thr	Val	Gly	Thr	Val	Asn	Val	Thr	Leu	Thr	Ile	Ala	Ala	Leu	Ala
				515				520					525		
Leu	Arg	Met	Ser	Asp	Thr	Leu	Lys	Lys	Glu	Val					
				530				535							

<210> 4  
<211> 27  
<212> PRT  
<213> Burkholderia cepacia

<400> 4  
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Pro Gly Phe Ala Arg Ala Ala Asp Ala Ala Asp  
20 25

<210> 5  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Artificial sequence; primer

<400> 5  
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<210> 6  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Artificial sequence; primer

<400> 6  
gagaagcttt ccgcacggtc agacttcc 28

<210> 7  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Artificial sequence; primer

<400> 7  
catgccatgg cacacaacga caacact 27

<210> 8  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Artificial sequence; primer

<400> 8  
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<210> 9  
<211> 16  
<212> PRT  
<213> Burkholderia cepacia

<400> 9  
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1 5 10 15

<210> 10  
<211> 25  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Artificial sequence; consensus

<221> UNSURE  
<222> (6)...(6)  
<223> Xaa=unknown

<221> UNSURE  
<222> (17)...(19)  
<223> Xaa=unknown

<221> UNSURE  
<222> (22)...(22)  
<223> Xaa=unknown

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1 5 10 15  
Xaa Xaa Xaa Asp Cys Xaa Ala Cys His  
20 25

<210> 11  
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<212> DNA  
<213> Burkholderia cepacia

<220>  
<221> CDS  
<222> (673)...(1950)

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agccgcgaag aagatccatc tgtcgaacat gtcccgcattc aaccaggaga cgcagaagat 180  
cttcaaggcc ggcaaactga tgaagcacgaa ggagctcgac ggcgcagatcc ggcaccgttc 240  
cgccgcgtac gtgcaggctcg actgcttcca cgagattctg cccgcggccg agaaccgcatt 300  
cgtgccgagc aagacgcca ccgacgcgtatcgatcccg cgcggccgaga tcacgtatgc 360  
gatcgacgtatcgatcccg aacgcgtatcgatcccg cgcggccgaga tcacgtatgc 420  
gatcgacgtatcgatcccg aacgcgtatcgatcccg cgcggccgaga tcacgtatgc 480  
gatcgacgtatcgatcccg aacgcgtatcgatcccg cgcggccgaga tcacgtatgc 540  
gatcgacgtatcgatcccg aacgcgtatcgatcccg cgcggccgaga tcacgtatgc 600  
gatcgacgtatcgatcccg aacgcgtatcgatcccg cgcggccgaga tcacgtatgc 660  
gatcgacgtatcgatcccg aacgcgtatcgatcccg cgcggccgaga tcacgtatgc 720  
Val Arg Lys Ser Thr Leu Thr Phe Leu Leu Ala Gly Cys  
1 5 10

ctc	gcf	ctg	ccc	ggc	ctc	gca	cgc	gcf	gcc	gat	tcg	gcc	gat	ccg	gcf		759
Leu	Ala	Leu	Pro	Gly	Leu	Ala	Arg	Ala	Ala	Asp	Ser	Ala	Asp	Pro	Ala		
15					20					25							
cat	gtc	aag	cgc	ggc	gaa	tac	ctc	gcc	gtc	gcf	ggc	gac	tgc	atg	gca		807
His	Val	Lys	Arg	Gly	Glu	Tyr	Leu	Ala	Val	Ala	Gly	Asp	Cys	Met	Ala		
30					35				40				45				
tgc	cac	acc	gcf	aag	ggc	aag	ccg	ttc	gcf	ggc	ggc	ctc	ggc	atg		855	
Cys	His	Thr	Ala	Lys	Gly	Gly	Lys	Pro	Phe	Ala	Gly	Gly	Leu	Gly	Met		
								50		55			60				
ccg	gtg	ccg	atg	ctc	ggc	aag	atc	tat	acg	agc	aac	atc	aca	ccg	gat		903
Pro	Val	Pro	Met	Leu	Gly	Lys	Ile	Tyr	Thr	Ser	Asn	Ile	Thr	Pro	Asp		
							65		70			75					
ccc	gat	acc	ggc	atc	ggc	aac	tgg	acg	ttc	gag	gac	ttc	gag	ccg	gcf		951
Pro	Asp	Thr	Gly	Ile	Gly	Asn	Trp	Thr	Phe	Glu	Asp	Phe	Glu	Arg	Ala		
						80		85		90							
gtg	cgf	cac	ggc	gta	tcg	aag	aac	ggc	gac	aac	ctg	tac	ccg	gcf	atg		999
Val	Arg	His	Gly	Val	Ser	Lys	Asn	Gly	Asp	Asn	Leu	Tyr	Pro	Ala	Met		
						95		100		105							
ccg	tac	gtg	tcg	tac	gcf	aag	atc	aac	gac	gac	gac	gtg	caa	gcf	ctg		1047
Pro	Tyr	Val	Ser	Tyr	Ala	Lys	Ile	Asn	Asp	Asp	Asp	Val	Gln	Ala	Leu		
						110		115		120			125				
tac	gcf	tac	tcc	atg	cac	ggc	gtc	gaa	ccg	gtc	aag	cag	gcf	ccg	ccg		1095
Tyr	Ala	Tyr	Phe	Met	His	Gly	Val	Glu	Pro	Val	Lys	Gln	Ala	Pro	Pro		
						130		135			140						
aag	aac	gag	atc	ccc	gcf	ctg	ctg	agc	atg	ccg	tgg	ccg	ctg	aag	atc		1143
Lys	Asn	Glu	Ile	Pro	Ala	Leu	Leu	Ser	Met	Arg	Trp	Pro	Leu	Lys	Ile		
						145		150		155							
tgg	aac	tgg	ctg	tcc	ctg	aag	gac	ggc	gtg	tac	cag	ccg	aag	ccc	gag		1191
Trp	Asn	Trp	Leu	Phe	Leu	Lys	Asp	Gly	Val	Tyr	Gln	Pro	Lys	Pro	Glu		
						160		165		170							
cag	agc	gcc	gag	tgg	aac	ccg	ggc	gcc	tat	ctc	gtg	cag	ggc	ctc	gcf		1239
Gln	Ser	Ala	Glu	Trp	Asn	Arg	Gly	Ala	Tyr	Leu	Val	Gln	Gly	Leu	Ala		
						175		180		185							
cac	tgc	agc	acg	tgc	cac	acg	ccg	cgc	atc	gcf	atg	cag	gag	aag		1287	
His	Cys	Ser	Thr	Cys	His	Thr	Pro	Arg	Gly	Ile	Ala	Met	Gln	Glu	Lys		
						190		195		200			205				
tcg	ctc	gac	gaa	acg	ggc	ggc	agc	ttc	ctg	tcg	ggc	tcg	gtg	ctc	gcf		1335
Ser	Leu	Asp	Glu	Thr	Gly	Gly	Ser	Phe	Leu	Ser	Gly	Ser	Val	Leu	Ala		
							210		215		220						
ggc	tgg	gac	ggc	tac	aac	atc	acg	tcc	gac	ccg	aac	gcf	ggg	atc	ggc		1383
Gly	Trp	Asp	Gly	Tyr	Asn	Ile	Thr	Ser	Asp	Pro	Asn	Ala	Gly	Ile	Gly		
						225		230		235							
ggc	tgg	acg	cag	cag	ctc	gtc	cag	tac	ctg	ccg	acc	ggc	agc	gtg		1431	

Gly	Trp	Thr	Gln	Gln	Gln	Leu	Val	Gln	Tyr	Leu	Arg	Thr	Gly	Ser	Val		
240																240	
ccg	ggc	ctc	gcg	cag	gcf	gcc	ccg	atg	gcc	gag	gcg	atc	gag	cac		1479	
Pro	Gly	Leu	Ala	Gln	Ala	Ala	Gly	Pro	Met	Ala	Glu	Ala	Ile	Glu	His		
255																255	
agc	tcc	tcg	aag	atg	acc	gaa	gcc	gac	atc	ggc	gag	gcg	atg	gcc	gag		1527
Ser	Phe	Ser	Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Gly	Pro	Met	Ala	Glu		
270																270	
275																275	
280																280	
285																285	
gcf	atc	gag	cac	agc	tcc	tcg	aag	atg	acc	gaa	gcc	gac	atc	ggc	cgf		1575
Ala	Ile	Glu	His	Ser	Phe	Ser	Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Arg		
290																290	
295																295	
300																300	
tcg	tcg	tgg	ggc	aag	ccg	gcc	gag	gat	ggc	ctg	aag	ctg	cgf	ggc	gtc		1623
Ser	Ser	Trp	Gly	Lys	Pro	Ala	Glu	Asp	Gly	Leu	Lys	Leu	Arg	Gly	Val		
305																305	
310																310	
315																315	
gcf	ctc	gcg	tcg	tcg	ggc	atc	gat	ccg	gca	ccg	ctg	tat	ctc	ggc	aac		1671
Ala	Leu	Ala	Ser	Ser	Gly	Ile	Asp	Pro	Ala	Pro	Leu	Tyr	Leu	Gly	Asn		
320																320	
325																325	
330																330	
tgc	gcf	acc	tgc	cac	cag	atg	cag	ggc	aag	ggc	acg	ccg	gac	ggf	tac		1719
Cys	Ala	Thr	Cys	His	Gln	Met	Gln	Gly	Lys	Gly	Thr	Pro	Asp	Gly	Tyr		
335																335	
340																340	
345																345	
tac	ccg	ccg	ttg	ttc	cac	aac	tcg	acg	gtc	ggc	gcf	tcg	aat	ccg	acc		1767
Tyr	Pro	Pro	Leu	Phe	His	Asn	Ser	Thr	Val	Gly	Ala	Ser	Asn	Pro	Thr		
350																350	
355																355	
360																360	
365																365	
aac	ctc	gtg	cag	gtg	atc	ctg	aac	ggc	gtg	cag	cgf	aag	gcc	ggc	agc		1815
Asn	Leu	Val	Gln	Val	Ile	Leu	Asn	Gly	Val	Gln	Arg	Lys	Ala	Gly	Ser		
370																370	
375																375	
380																380	
gag	gac	gtc	ggg	atg	ccc	gcf	ttc	cgf	cac	gag	ctg	tcg	aat	ccg	acc		1863
Glu	Asp	Val	Gly	Met	Pro	Ala	Phe	Arg	His	Glu	Leu	Ser	Asp	Ala	Gln		
385																385	
390																390	
395																395	
atc	gcc	gcg	ctg	acg	aac	tac	ctg	acg	ggg	cag	ttc	ggc	aat	ccg	gcc		1911
Ile	Ala	Ala	Leu	Thr	Asn	Tyr	Leu	Thr	Gly	Gln	Phe	Gly	Asn	Pro	Ala		
400																400	
405																405	
410																410	
gcf	aag	gtg	acc	gag	cag	gac	gtc	gcf	aag	ctg	cgf	tga	aacgcggcac		1960		
Ala	Lys	Val	Thr	Glu	Gln	Asp	Val	Ala	Lys	Leu	Arg	*					
415																415	
420																420	
425																425	
gcggcgaggc	agggcaaca	aaa	tagaaaagag	gaggagcaca	gcacatcggg	cgcccccg										2020	
tgccgggtgt	tgcagagcgg	gacggggcggc	gcaggcggtc	gccccgtcctg	gttcacaggc											2080	
aatccgggtc	gcccacggcc	cgcatcggtt	tcgttgatcg	agaccatgac	accgaaccaa											2140	
ccgtttctcg	cgtcccacgc	cgatgtgctg	ctgctgtgt	cccgaatcct	gctcgatgc											2200	
ctgttcgtga	tgttcggctg	gaagaagatt	atcgacttct	ccggatcgat	cgccgttcatg											2260	
ggcagcgagg	gcccgcggc	gccgatcatc	tcggccggcga	tctccgtcgt	gatggagctc											2320	
atcgtcggga	ttgcgatcct	cgtcgggttc	cagacgcggc	cgctcgccgt	gttgcttgcg											2380	
ctgtacacgca	tcggtaaccgg	catcatcgcc														2410	

<211> 425

<212> PRT

<213> Burkholderia cepacia

<400> 12

Val Arg Lys Ser Thr Leu Thr Phe Leu Leu Ala Gly Cys Leu Ala Leu  
1 5 10 15  
Pro Gly Leu Ala Arg Ala Ala Asp Ser Ala Asp Pro Ala His Val Lys  
20 25 30  
Arg Gly Glu Tyr Leu Ala Val Ala Gly Asp Cys Met Ala Cys His Thr  
35 40 45  
Ala Lys Gly Lys Pro Phe Ala Gly Gly Leu Gly Met Pro Val Pro  
50 55 60  
Met Leu Gly Lys Ile Tyr Thr Ser Asn Ile Thr Pro Asp Pro Asp Thr  
65 70 75 80  
Gly Ile Gly Asn Trp Thr Phe Glu Asp Phe Glu Arg Ala Val Arg His  
85 90 95  
Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met Pro Tyr Val  
100 105 110  
Ser Tyr Ala Lys Ile Asn Asp Asp Val Gln Ala Leu Tyr Ala Tyr  
115 120 125  
Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro Lys Asn Glu  
130 135 140  
Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile Trp Asn Trp  
145 150 155 160  
Leu Phe Leu Lys Asp Gly Val Tyr Gln Pro Lys Pro Glu Gln Ser Ala  
165 170 175  
Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala His Cys Ser  
180 185 190  
Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys Ser Leu Asp  
195 200 205  
Glu Thr Gly Gly Ser Phe Leu Ser Gly Ser Val Leu Ala Gly Trp Asp  
210 215 220  
Gly Tyr Asn Ile Thr Ser Asp Pro Asn Ala Gly Ile Gly Gly Trp Thr  
225 230 235 240  
Gln Gln Leu Val Gln Tyr Leu Arg Thr Gly Ser Val Pro Gly Leu  
245 250 255  
Ala Gln Ala Ala Gly Pro Met Ala Glu Ala Ile Glu His Ser Phe Ser  
260 265 270  
Lys Met Thr Glu Ala Asp Ile Gly Gly Pro Met Ala Glu Ala Ile Glu  
275 280 285  
His Ser Phe Ser Lys Met Thr Glu Ala Asp Ile Gly Arg Ser Ser Trp  
290 295 300  
Gly Lys Pro Ala Glu Asp Gly Leu Lys Leu Arg Gly Val Ala Leu Ala  
305 310 315 320  
Ser Ser Gly Ile Asp Pro Ala Pro Leu Tyr Leu Gly Asn Cys Ala Thr  
325 330 335  
Cys His Gln Met Gln Gly Lys Gly Thr Pro Asp Gly Tyr Tyr Pro Pro  
340 345 350  
Leu Phe His Asn Ser Thr Val Gly Ala Ser Asn Pro Thr Asn Leu Val  
355 360 365  
Gln Val Ile Leu Asn Gly Val Gln Arg Lys Ala Gly Ser Glu Asp Val  
370 375 380  
Gly Met Pro Ala Phe Arg His Glu Leu Ser Asp Ala Gln Ile Ala Ala  
385 390 395 400  
Leu Thr Asn Tyr Leu Thr Gly Gln Phe Gly Asn Pro Ala Ala Lys Val  
405 410 415

Thr Glu Gln Asp Val Ala Lys Leu Arg  
420 425

<210> 13  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Artificial sequence; primer

<400> 13  
tgccaccgtgc ggaaatctac tctcact 27

<210> 14  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Artificial sequence; primer

<400> 14  
acttccttct tcagcgtgtc cgacatc 27

<210> 15  
<211> 1441  
<212> DNA  
<213> Burkholderia cepacia

<220>  
<221> CDS  
<222> (121) ... (1398)

<400> 15  
tccgaacctg ttcatttcga gcagcgcgac gatgccgacc gtcggtaccc taaacgtgac 60  
gctgacgatc gccgcgtcg cgctgcggat gtcggacacg ctgaagaagg aagtctgacc 120  
gtg cgg aaa tct act ctc act ttc ctc atc gcc ggc tgc ctc gcg ttg 168  
Val Arg Lys Ser Thr Leu Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu  
1 5 10 15

ccg ggc ttc gcg cgc gcg gcc gat gcg gcc gat ccg gcg ctg gtc aag 216  
Pro Gly Phe Ala Arg Ala Ala Asp Ala Ala Asp Pro Ala Leu Val Lys  
20 25 30

cgc ggc gaa tac ctc gcg acc gcc atg ccg gta ccg atg ctc ggc aag 264  
Arg Gly Glu Tyr Leu Ala Thr Ala Met Pro Val Pro Met Leu Gly Lys  
35 40 45

atc tac acg agc aac atc acg ccc gat ccc gat acg ggc gac tgc atg 312  
Ile Tyr Thr Ser Asn Ile Thr Pro Asp Pro Asp Thr Gly Asp Cys Met  
50 55 60

gcc tgc cac acc gtg aag ggc ggc aag ccg tac gcg ggc ggc ctt ggc 360  
Ala Cys His Thr Val Lys Gly Gly Lys Pro Tyr Ala Gly Gly Leu Gly  
65 70 75 80

ggc atc ggc aaa tgg acg ttc gag gac ttc gag cgc gcg gtg cg	cac	408	
Gly Ile Gly Lys Trp Thr Phe Glu Asp Phe Glu Arg Ala Val Arg His			
85	90	95	
ggc gtg tcg aag aac ggc gac aac ctg tat ccg gcg atg ccg tac gtg		456	
Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met Pro Tyr Val			
100	105	110	
tcg tac gcg aag atc aag gac gac gta cgc gcg ctg tac gcc tac		504	
Ser Tyr Ala Lys Ile Lys Asp Asp Asp Val Arg Ala Leu Tyr Ala Tyr			
115	120	125	
ttc atg cac ggc gtc gag ccg gtc aag cag gcg ccg aag aac gag		552	
Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro Lys Asn Glu			
130	135	140	
atc cca gcg ctg cta agc atg cgc tgg ccg ctg aag atc tgg aac tgg		600	
Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile Trp Asn Trp			
145	150	155	160
ctg ttc ctg aag gac ggc ccg tac cag ccg aag ccg tcg cag agc g	cc	648	
Leu Phe Leu Lys Asp Gly Pro Tyr Gln Pro Lys Pro Ser Gln Ser Ala			
165	170	175	
gaa tgg aat cgc ggc gcg tat ctg gtg cag ggt ctc gcg cac tgc agc		696	
Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala His Cys Ser			
180	185	190	
acg tgc cac acg ccg cgc ggc atc gcg atg cag gag aag tcg ctc gac		744	
Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys Ser Leu Asp			
195	200	205	
gaa acc ggc ggc agc ttc ctc gcg ggg tcg gtg ctc gcc ggc tgg gac		792	
Glu Thr Gly Gly Ser Phe Leu Ala Gly Ser Val Leu Ala Gly Trp Asp			
210	215	220	
ggc tac aac atc acg tcg gac ccg aat gcg ggg atc ggc agc tgg acg		840	
Gly Tyr Asn Ile Thr Ser Asp Pro Asn Ala Gly Ile Gly Ser Trp Thr			
225	230	235	240
cag cag cag ctc gtg cag tat ttg cgc acc ggc agc gtg ccg ggc g	tc	888	
Gln Gln Leu Val Gln Tyr Leu Arg Thr Gly Ser Val Pro Gly Val			
245	250	255	
gcg cag gcg gcc ggg ccg atg gcc gag gcg gtc gag cac agc ttc tcg		936	
Ala Gln Ala Ala Gly Pro Met Ala Glu Ala Val Glu His Ser Phe Ser			
260	265	270	
aag atg acc gaa gcg gac atc ggt gcg atc gcc acg tac gtc cgc acg		984	
Lys Met Thr Glu Ala Asp Ile Gly Ala Ile Ala Thr Tyr Val Arg Thr			
275	280	285	
gtg ccg gcc gtt gcc gac agc aac gcg aag cag ccg cgg tcg tcg tgg		1032	
Val Pro Ala Val Ala Asp Ser Asn Ala Lys Gln Pro Arg Ser Ser Trp			
290	295	300	

ggc aag ccg gcc gag gac ggg ctg aag ctg cgc ggt gtc gcg ctc gcg		1080
Gly Lys Pro Ala Glu Asp Gly Leu Lys Leu Arg Gly Val Ala Leu Ala		
305	310	315
320		
tcg tcg ggc atc gat ccg gcg cgg ctg tat ctc ggc aac tgc gcg acg		1128
Ser Ser Gly Ile Asp Pro Ala Arg Leu Tyr Leu Gly Asn Cys Ala Thr		
325	330	335
tgc cac cag atg cag ggc aag ggc acg ccg gac ggc tat tac ccg tcg		1176
Cys His Gln Met Gln Gly Lys Gly Thr Pro Asp Gly Tyr Tyr Pro Ser		
340	345	350
ctg ttc cac aac tcc acc gtc ggc gcg tcg aat ccg tcg aac ctc gtg		1224
Leu Phe His Asn Ser Thr Val Gly Ala Ser Asn Pro Ser Asn Leu Val		
355	360	365
cag gtg atc ctg aac ggc gtg cag cgc aag atc ggc agc gag gat atc		1272
Gln Val Ile Leu Asn Gly Val Gln Arg Lys Ile Gly Ser Glu Asp Ile		
370	375	380
ggg atg ccc gct ttc cgc tac gat ctg aac gac ggc cag atc gcc gcg		1320
Gly Met Pro Ala Phe Arg Tyr Asp Leu Asn Asp Ala Gln Ile Ala Ala		
385	390	395
400		
ctg acg aac tac gtg acc gcg cag ttc ggc aat ccg gcg gcg aag gtg		1368
Leu Thr Asn Tyr Val Thr Ala Gln Phe Gly Asn Pro Ala Ala Lys Val		
405	410	415
acg gag cag gac gtc gcg aag ctg cgc tga catagtcggg cgcgccgaca		1418
Thr Glu Gln Asp Val Ala Lys Leu Arg *		
420	425	
cggcgcaacc gataggacag gag		1441
<210> 16		
<211> 425		
<212> PRT		
<213> Burkholderia cepacia		
<400> 16		
Val Arg Lys Ser Thr Leu Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu		
1 5 10 15		
Pro Gly Phe Ala Arg Ala Ala Asp Ala Ala Asp Pro Ala Leu Val Lys		
20 25 30		
Arg Gly Glu Tyr Leu Ala Thr Ala Met Pro Val Pro Met Leu Gly Lys		
35 40 45		
Ile Tyr Thr Ser Asn Ile Thr Pro Asp Pro Asp Thr Gly Asp Cys Met		
50 55 60		
Ala Cys His Thr Val Lys Gly Gly Lys Pro Tyr Ala Gly Gly Leu Gly		
65 70 75 80		
Gly Ile Gly Lys Trp Thr Phe Glu Asp Phe Glu Arg Ala Val Arg His		
85 90 95		
Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met Pro Tyr Val		
100 105 110		
Ser Tyr Ala Lys Ile Lys Asp Asp Asp Val Arg Ala Leu Tyr Ala Tyr		
115 120 125		
Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro Lys Asn Glu		

130	135	140
Ile Pro Ala Leu Leu Ser Met Arg Trp Pro	Leu Lys Ile Trp Asn Trp	
145	150	155 160
Leu Phe Leu Lys Asp Gly Pro Tyr Gln Pro	Lys Pro Ser Gln Ser Ala	
165	170	175
Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln	Gly Leu Ala His Cys Ser	
180	185	190
Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln	Glu Lys Ser Leu Asp	
195	200	205
Glu Thr Gly Gly Ser Phe Leu Ala Gly Ser Val	Leu Ala Gly Trp Asp	
210	215	220
Gly Tyr Asn Ile Thr Ser Asp Pro Asn Ala	Gly Ile Gly Ser Trp Thr	
225	230	235 240
Gln Gln Gln Leu Val Gln Tyr Leu Arg Thr	Gly Ser Val Pro Gly Val	
245	250	255
Ala Gln Ala Ala Gly Pro Met Ala Glu Ala Val	Glu His Ser Phe Ser	
260	265	270
Lys Met Thr Glu Ala Asp Ile Gly Ala Ile Ala	Thr Tyr Val Arg Thr	
275	280	285
Val Pro Ala Val Ala Asp Ser Asn Ala Lys	Gln Pro Arg Ser Ser Trp	
290	295	300
Gly Lys Pro Ala Glu Asp Gly Leu Lys Leu Arg	Gly Val Ala Leu Ala	
305	310	315 320
Ser Ser Gly Ile Asp Pro Ala Arg Leu Tyr	Leu Gly Asn Cys Ala Thr	
325	330	335
Cys His Gln Met Gln Gly Lys Gly Thr Pro Asp	Gly Tyr Tyr Pro Ser	
340	345	350
Leu Phe His Asn Ser Thr Val Gly Ala Ser Asn	Pro Ser Asn Leu Val	
355	360	365
Gln Val Ile Leu Asn Gly Val Gln Arg Lys Ile	Gly Ser Glu Asp Ile	
370	375	380
Gly Met Pro Ala Phe Arg Tyr Asp Leu Asn Asp	Ala Gln Ile Ala Ala	
385	390	395 400
Leu Thr Asn Tyr Val Thr Ala Gln Phe Gly Asn	Pro Ala Ala Lys Val	
405	410	415
Thr Glu Gln Asp Val Ala Lys Leu Arg		
420	425	

<210> 17  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Artificial sequence; heme binding motif

<221> UNSURE  
<222> (2)...(3)  
<223> Xaa=unknown

<400> 17  
Cys Xaa Xaa Cys His  
1 5

<210> 18

<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Artificial sequence; primer

<400> 18  
catgccatgg cacacaacga caacact

27

<210> 19  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Artificial sequence; primer

<400> 19  
cccaagcttg ggtcagactt ctttcag c

31